SEQUENCE LISTING

<110> ITO, Yasuaki
     FUJII, Ryo
     KOBAYASHI, Makoto
     HINUMA, Shuji
     HASHIMOTO, Tadatoshi
     TANAKA, Yasuhiro

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<141> 2005-10-12

<150> PCT/JP2004/005947
<151> 2004-04-23

<150> JP 2003-122464
<151> 2003-04-25

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         35   40   45
Ser Ala Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu
    50   55   60
Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile
65   70   75   80
Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp
         85   90   95
Asn Pro Leu Thr Thr Ser Ser Tyr Thr Leu Ser Cys Lys Leu His Thr
         100   105   110
Phe Leu Phe Glu Ala Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr
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Leu Ser Phe Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys
         130   135   140
Ala Val Ser Gly Pro Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp
145   150   155   160
Val Thr Ser Ala Leu Val Ala Leu Pro Leu Leu Phe Ala Met Gly Thr
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Glu Tyr Pro Leu Val Asn Val Pro Ser His Arg Gly Leu Thr Cys Asn
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Arg Ser Ser Thr Arg His His Glu Gln Pro Glu Thr Ser Asn Met Ser
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Ile Cys Thr Asn Leu Ser Ser Arg Trp Thr Val Phe Gln Ser Ser Ile

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                    245                  250                  255
Leu Ala Gly Gly Thr Arg Pro Pro Gln Leu Arg Lys Ser Glu Ser Glu
                260                  265                  270
Glu Ser Arg Thr Ala Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile
            275                  280                  285
Val Val Thr Leu Ala Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile
            290                  295                  300
Met Ala Ala Ala Lys Pro Lys His Asp Trp Thr Arg Ser Tyr Phe Arg
305                  310                  315                  320
Ala Tyr Met Ile Leu Leu Pro Phe Ser Glu Thr Phe Phe Tyr Leu Ser
                325                  330                  335
Ser Val Ile Asn Pro Leu Leu Tyr Thr Val Ser Ser Gln Gln Phe Arg
            340                  345                  350
Arg Val Phe Val Gln Val Leu Cys Cys Arg Leu Ser Leu Gln His Ala
            355                  360                  365
Asn His Glu Lys Arg Leu Arg Val His Ala His Ser Thr Thr Asp Ser
    370                  375                  380
Ala Arg Phe Val Gln Arg Pro Leu Leu Phe Ala Ser Arg Arg Gln Ser
385                  390                  395                  400
Ser Ala Arg Arg Thr Glu Lys Ile Phe Leu Ser Thr Phe Gln Ser Glu
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Ala Glu Pro Gln Ser Lys Ser Gln Ser Leu Ser Leu Glu Ser Leu Glu
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<213> Mouse

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                 20                  25                  30
Leu Ile Leu Val Tyr Leu Ile Ile Phe Val Val Gly Ile Leu Gly Asn
           35                  40                  45
Ser Val Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu
      50                  55                  60
Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile
 65                  70                  75                  80
Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp
                 85                  90                  95
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3

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Asn Pro Leu Thr Thr Pro Ser Tyr Ala Leu Ser Cys Lys Leu His Thr
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Phe Leu Phe Glu Thr Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr
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Leu Ser Phe Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Lys Tyr Lys
        130             135             140
Ala Val Ser Gly Pro Arg Gln Val Lys Leu Leu Ile Gly Phe Val Trp
145             150             155             160
Val Thr Ser Ala Leu Val Ala Leu Pro Leu Leu Phe Ala Met Gly Ile
            165             170             175
Glu Tyr Pro Leu Val Asn Val Pro Thr His Lys Gly Leu Asn Cys Asn
        180             185             190
Leu Ser Arg Thr Arg His His Asp Glu Pro Gly Asn Ser Asn Met Ser
        195             200             205
Ile Cys Thr Asn Leu Ser Asn Arg Trp Glu Val Phe Gln Ser Ser Ile
    210             215             220
Phe Gly Ala Phe Ala Val Tyr Leu Val Val Leu Ala Ser Val Ala Phe
225             230             235             240
Met Cys Trp Asn Met Met Lys Val Leu Met Lys Ser Lys Gln Gly Thr
            245             250             255
Leu Ala Gly Thr Gly Pro Gln Leu Gln Leu Arg Lys Ser Glu Ser Glu
            260             265             270
Glu Ser Arg Thr Ala Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile
        275             280             285
Val Val Thr Leu Ala Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile
    290             295             300
Met Ala Ala Ala Lys Pro Lys His Asp Trp Thr Arg Thr Tyr Phe Arg
305             310             315             320
Ala Tyr Met Ile Leu Leu Pro Phe Ser Asp Thr Phe Phe Tyr Leu Ser
            325             330             335
Ser Val Val Asn Pro Leu Leu Tyr Asn Val Ser Ser Gln Gln Phe Arg
            340             345             350
Lys Val Phe Trp Gln Val Leu Cys Cys Arg Leu Thr Leu Gln His Ala
        355             360             365
Asn Gln Glu Lys Arg Gln Arg Ala Arg Phe Ile Ser Thr Lys Asp Ser
    370             375             380
Thr Ser Ser Ala Arg Ser Pro Leu Ile Phe Leu Ala Ser Arg Arg Ser
385             390             395             400
Asn Ser Ser Ser Arg Arg Thr Asn Lys Val Phe Leu Ser Thr Phe Gln
            405             410             415
Thr Glu Ala Lys Pro Gly Glu Ala Lys Pro Gln Pro Leu Ser Pro Glu
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<211> 1368
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<213> Mouse

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4

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            20                  25                  30
Leu Thr Leu Val Tyr Leu Ile Val Phe Val Val Gly Ile Leu Gly Asn
        35                  40                  45
Ser Val Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu
    50                  55                  60
Gln Lys Glu Val Thr Asp His Met Ile Ser Leu Ala Cys Ser Asp Ile
65                  70                  75                  80
Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp
                85                  90                  95
Asn Pro Leu Thr Thr Pro Ser Tyr Ala Leu Ser Cys Lys Leu His Thr
            100                 105                 110
Phe Leu Phe Glu Thr Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr
        115                 120                 125
Leu Ser Phe Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys
    130                 135                 140
Asp Val Ser Gly Pro Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp
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Val Thr Ser Ala Leu Val Ala Leu Pro Leu Leu Phe Ala Met Gly Ile
                165                 170                 175
Glu Tyr Pro Leu Ala Asn Val Pro Thr His Lys Gly Leu Asn Cys Asn
            180                 185                 190
Leu Ser Arg Thr Arg His His Asp His Pro Gly Asp Ser Asn Met Ser
            195                 200                 205
Ile Cys Thr Asn Leu Ser Ser Arg Trp Glu Val Phe Gln Ser Ser Ile
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Phe Gly Ala Phe Ala Val Tyr Leu Val Val Leu Val Ser Val Ala Phe
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5

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Met Ala Ala Ala Lys Pro Lys His Asp Trp Thr Lys Ser Tyr Phe Lys
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Ala Tyr Met Ile Leu Leu Pro Phe Ser Asp Thr Phe Phe Tyr Leu Ser
                       325                            330                            335
Ser Val Val Asn Pro Leu Leu Tyr Asn Val Ser Ser Gln Gln Phe Arg
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Lys Val Phe Trp Gln Val Leu Cys Cys Arg Leu Thr Leu Gln His Ala
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Asn Gln Glu Lys Gln Gln Arg Ala Tyr Phe Ser Ser Thr Lys Asn Ser
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Ser Arg Ser Ala Arg Ser Pro Leu Ile Phe Leu Ala Ser Arg Arg Ser
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Asn Ser Ser Ser Arg Arg Thr Asn Lys Val Phe Leu Ser Thr Phe Gln
                       405                            410                            415
Ala Glu Ala Lys Pro Leu Glu Gly Glu His Gln Pro Leu Ser Pro Glu
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Ser Pro Gln Thr Gly Ser Glu Thr Lys Pro Ala Gly Ser Ala Thr Glu
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6

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7

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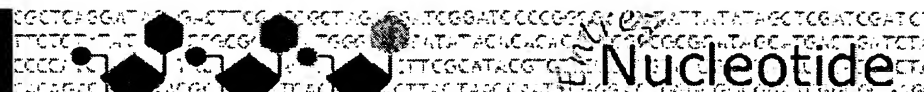
NCBI   Nucleotide

PubMed   Nucleotide   Protein   Genome   Structure   PMC   Taxonomy   OMIM   Books

Search [Nucleotide ▾] for [   ] [Go] [Clear]

Limits   Preview/Index   History   Clipboard   Details

Display [GenBank ▾] Show [5 ▾] [Send to ▾]

Range: from [begin   ] to [end   ]   ☐ Reverse complemented strand   Features: ☐ SNP ☑ CDD ☐

☐ **1:** XM_222578. Reports PREDICTED: Rattus...[gi:34879487]   Links

Comment   Features   Sequence

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ACCESSION   XM_222578
VERSION     XM_222578.2  GI:34879487
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
COMMENT     MODEL REFSEQ:  This record is predicted by automated computational
            analysis. This record is derived from an annotated genomic sequence
            (NW_047393) using gene prediction method: GNOMON, supported by mRNA
            evidence.
            Also see:
                Documentation of NCBI's Annotation Process

            On Sep 22, 2003 this sequence version replaced gi:27676303.
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     1321 aaacctgctg gttccgccac agaaaatagt ttacaggagc aggaagtgtg a
//
```

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